

SEQUENCE LISTING

<110> Dean, Michael
Allikmets, Rando
Hutchinson, Amy A.

<120> ATP-BINDING TRANSPORTER (ABC7) AND METHODS FOR DETECTION OF ANEMIA AND ATAXIA

<130> 4239-67289

<150> US 09/422,840

<151> 1999-10-21

<150> US 60/105,497

<151> 1998-10-23

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 2345

<212> DNA

<213> Homo sapien

<400> 1

```
atggcgctgc tcgcgatgca ttcttggcgc tgggcggccg cggcggctgc tttcgaaaag      60
cgccggcact ccgcgattct gatccggcct ttagtctctg ttagcggctc aggtccgcag      120
tggaggccac atcaactcgg cgccttggga accgctcgag cctaccagat tccagagtca      180
ttaaaaagta tcacatggca gagattggga aaaggcaatt caggacagtt cttagatgct      240
gcaaaggctc tccaggtatg gccactgata gaaaagagga catgttggca tggtcatgca      300
ggaggaggac tccacacaga cccaaaagaa gggttaaaag atgttgatac tcggaaaatc      360
ataaaagcaa tgctttctta tgtgtggccc aaagacaggc cagatctacg agctagagtt      420
gccatttcgc tgggattttt gggtggtgca aaggccatga atatttggtt tcccttcatg      480
tttaaatatg ctgtagacag cctcaaccag atgtcgggaa acatgctgaa cctgagtgat      540
gcaccaaata cagttgcaac catggcaaca gcagttctga ttggctatgg tgtatcaaga      600
gctggagctg ctttttttaa cgaagttcga aatgcagtat ttggcaaggt agcccagaat      660
tcaatccgaa gaatagccaa aaatgtcttt ctccatcttc acaacctgga tctgggtttt      720
cacctgagca gacagacggg agctttatct aaggctattg acagaggaac aaagggatc      780
agttttgtcc tgagtgcttt ggtatttaat cttcttccca tcatgtttga agtgatgctt      840
gtcagtggtg ttttgtatta caaatgcggt gccagtttg ctttggtaac ctttgggaaca      900
```

cttggtacat acacagcatt cacagttgca gtcacacggt ggagaactag atttagaata	960
gaaatgaaca aagcagataa tgatgcaggt aatgctgcta tagactcact gctgaattat	1020
gaaactgtga agtatttttaa taatgaaaga tatgaagcac agagatatga tggatttttg	1080
aagacgtatg agactgcttc attgaaaagt acctctactc tggctatgct gaactttgggt	1140
caaagtgcta ttttcagtgt cggtttaaca gctataatgg tgctcgccag tcaggggaatt	1200
gtggcaggta cccttactgt tggagatcta gtaatggtga atggactgct ttttcagctt	1260
tcattacccc tgaactttct gggaaactgta tatagagaga ctagacaagc actcatagat	1320
atgaacacct tgtttactct actcaaggta gacacccaaa ttaaagacaa agtgatggca	1380
tctccccttc agatcacacc acagacagct accgtggcct ttgataatgt gcattttgaa	1440
tacattgagg gccagaaagt ccttagtgga atatcctttg aagtccttgc aggaaagaaa	1500
gtggccattg taggaggtag tgggtcaggg aaaagcacia tagtgaggct attatttcgc	1560
ttctatgagc ctcaaaaggg tagcatttat cttgctggtc aaaatataca agatgtgagc	1620
ctggaaagcc ttcggagggc agtgggagtg gtacctcagg atgctgtcct cttccataat	1680
actattttatt acaacctctt atatggaaac atcagtgcct cacctgagga agtgtatgca	1740
gtggcaaaat tagctggact tcatgatgca attcttcgaa tgccacatgg atatgacacc	1800
caagtagggg aacgaggact caagctttca ggaggagaaa agcaaagagt agcaattgca	1860
agagccattt tgaaggaccc cccagtcata ctctatgatg aagctacttc atcgttagat	1920
tcgattactg aagagactat tcttggtgcc atgaaggatg tggtaaaca cagaacttct	1980
attttcattg cacacagatt gtcaacagtg gttgatgcag atgaaatcat tgtcttggat	2040
cagggtaaag tagccgaacg tggtaaccac catggtttgc ttgctaacc tcatagtatc	2100
tattcagaaa tgtggcatac acagagcagc cgtgtgcaga accatgataa ccccaaattg	2160
gaagcaaaga aagaaaatat atccaaagag gaggaagaa agaaactaca agaagaaatt	2220
gtcaatagtg tgaaaggctg tggaaactgt tcgtgctaag tcacataaga cattttcttt	2280
ttttgttgtt ttggactaca tatttgcact gaagcagaat tgttttatta aaaaaatcat	2340
acatt	2345

<210> 2
 <211> 747
 <212> PRT
 <213> Homo sapien

 <400> 2

Met His Ser Trp Arg Trp Ala Ala Ala Ala Ala Phe Glu Lys Arg
 1 5 10 15

Arg His Ser Ala Ile Leu Ile Arg Pro Leu Val Ser Val Ser Gly Ser
 20 25 30

Gly Pro Gln Trp Arg Pro His Gln Leu Gly Ala Leu Gly Thr Ala Arg
 35 40 45

Ala Tyr Gln Ile Pro Glu Ser Leu Lys Ser Ile Thr Trp Gln Arg Leu
 50 55 60

Gly Lys Gly Asn Ser Gly Gln Phe Leu Asp Ala Ala Lys Ala Leu Gln
 65 70 75 80

Val Trp Pro Leu Ile Glu Lys Arg Thr Cys Trp His Gly His Ala Gly
 85 90 95

Gly Gly Leu His Thr Asp Pro Lys Glu Gly Leu Lys Asp Val Asp Thr
 100 105 110

Arg Lys Ile Ile Lys Ala Met Leu Ser Tyr Val Trp Pro Lys Asp Arg
 115 120 125

Pro Asp Leu Arg Ala Arg Val Ala Ile Ser Leu Gly Phe Leu Gly Gly
 130 135 140

Ala Lys Ala Met Asn Ile Val Val Pro Phe Met Phe Lys Tyr Ala Val
 145 150 155 160

Asp Ser Leu Asn Gln Met Ser Gly Asn Met Leu Asn Leu Ser Asp Ala
 165 170 175

Pro Asn Thr Val Ala Thr Met Ala Thr Ala Val Leu Ile Gly Tyr Gly
 180 185 190

Val Ser Arg Ala Gly Ala Ala Phe Phe Asn Glu Val Arg Asn Ala Val
 195 200 205

Phe Gly Lys Val Ala Gln Asn Ser Ile Arg Arg Ile Ala Lys Asn Val
 210 215 220

Phe Leu His Leu His Asn Leu Asp Leu Gly Phe His Leu Ser Arg Gln
 225 230 235 240

Thr Gly Ala Leu Ser Lys Ala Ile Asp Arg Gly Thr Lys Gly Ile Ser
 245 250 255

Phe Val Leu Ser Ala Leu Val Phe Asn Leu Leu Pro Ile Met Phe Glu
 260 265 270

Val Met Leu Val Ser Gly Val Leu Tyr Tyr Lys Cys Gly Ala Gln Phe
 275 280 285

Ala Leu Val Thr Leu Gly Thr Leu Gly Thr Tyr Thr Ala Phe Thr Val
 290 295 300

Ala Val Thr Arg Trp Arg Thr Arg Phe Arg Ile Glu Met Asn Lys Ala
 305 310 315 320

Asp Asn Asp Ala Gly Asn Ala Ala Ile Asp Ser Leu Leu Asn Tyr Glu
 325 330 335

Thr Val Lys Tyr Phe Asn Asn Glu Arg Tyr Glu Ala Gln Arg Tyr Asp
 340 345 350

Gly Phe Leu Lys Thr Tyr Glu Thr Ala Ser Leu Lys Ser Thr Ser Thr
 355 360 365

Leu Ala Met Leu Asn Phe Gly Gln Ser Ala Ile Phe Ser Val Gly Leu
 370 375 380

Thr Ala Ile Met Val Leu Ala Ser Gln Gly Ile Val Ala Gly Thr Leu
 385 390 395 400

Thr Val Gly Asp Leu Val Met Val Asn Gly Leu Leu Phe Gln Leu Ser
 405 410 415

Leu Pro Leu Asn Phe Leu Gly Thr Val Tyr Arg Glu Thr Arg Gln Ala
 420 425 430

Leu Ile Asp Met Asn Thr Leu Phe Thr Leu Leu Lys Val Asp Thr Gln
 435 440 445

Ile Lys Asp Lys Val Met Ala Ser Pro Leu Gln Ile Thr Pro Gln Thr

450		455		460
Ala Thr Val Ala Phe Asp Asn Val His Phe Glu Tyr Ile Glu Gly Gln				
465		470		475 480
Lys Val Leu Ser Gly Ile Ser Phe Glu Val Pro Ala Gly Lys Lys Val				
	485		490	495
Ala Ile Val Gly Gly Ser Gly Ser Gly Lys Ser Thr Ile Val Arg Leu				
	500		505	510
Leu Phe Arg Phe Tyr Glu Pro Gln Lys Gly Ser Ile Tyr Leu Ala Gly				
	515		520	525
Gln Asn Ile Gln Asp Val Ser Leu Glu Ser Leu Arg Arg Ala Val Gly				
	530		535	540
Val Val Pro Gln Asp Ala Val Leu Phe His Asn Thr Ile Tyr Tyr Asn				
545		550		555 560
Leu Leu Tyr Gly Asn Ile Ser Ala Ser Pro Glu Glu Val Tyr Ala Val				
	565		570	575
Ala Lys Leu Ala Gly Leu His Asp Ala Ile Leu Arg Met Pro His Gly				
	580		585	590
Tyr Asp Thr Gln Val Gly Glu Arg Gly Leu Lys Leu Ser Gly Gly Glu				
	595		600	605
Lys Gln Arg Val Ala Ile Ala Arg Ala Ile Leu Lys Asp Pro Pro Val				
	610		615	620
Ile Leu Tyr Asp Glu Ala Thr Ser Ser Leu Asp Ser Ile Thr Glu Glu				
625		630		635 640
Thr Ile Leu Gly Ala Met Lys Asp Val Val Lys His Arg Thr Ser Ile				
	645		650	655
Phe Ile Ala His Arg Leu Ser Thr Val Val Asp Ala Asp Glu Ile Ile				
	660		665	670
Val Leu Asp Gln Gly Lys Val Ala Glu Arg Gly Thr His His Gly Leu				
	675		680	685

Leu Ala Asn Pro His Ser Ile Tyr Ser Glu Met Trp His Thr Gln Ser
690 695 700

Ser Arg Val Gln Asn His Asp Asn Pro Lys Trp Glu Ala Lys Lys Glu
705 710 715 720

Asn Ile Ser Lys Glu Glu Glu Arg Lys Lys Leu Gln Glu Glu Ile Val
725 730 735

Asn Ser Val Lys Gly Cys Gly Asn Cys Ser Cys
740 745

<210> 3
<211> 2345
<212> DNA
<213> Homo sapien

<400> 3
atggcgctgc tcgcgatgca ttcttggcgc tgggcggccg cggcggctgc tttcgaaaag 60
cgccggcact ccgcgattct gatccggcct ttagtctctg ttagcggctc aggtccgcag 120
tggaggccac atcaactcgg cgccttggga accgctcgag cctaccagat tccagagtca 180
ttaaaaagta tcacatggca gagattggga aaaggcaatt caggacagtt cttagatgct 240
gcaaaggctc tccaggtatg gccactgata gaaaagagga catgttggca tggtcatgca 300
ggaggaggac tccacacaga cccaaaagaa gggttaaaag atgttgatac tcggaaaatc 360
ataaaagcaa tgctttctta tgtgtggccc aaagacaggc cagatctacg agctagagtt 420
gccatttcgc tgggattttt ggggtgtgca aaggccatga atattgtggt tcccttcatg 480
tttaaatatg ctgtagacag cctcaaccag atgtcgggaa acatgctgaa cctgagtgat 540
gcaccaaata cagttgcaac catggcaaca gcagttctga ttggctatgg tgtatcaaga 600
gctggagctg ctttttttaa cgaagttcga aatgcagtat ttggcaaggt agcccagaat 660
tcaatccgaa gaatagccaa aaatgtcttt ctccatcttc acaacctgga tctgggtttt 720
cacctgagca gacagacggg agctttatct aaggctattg acagaggaac aaagggtatc 780
agttttgtcc tgagtgtctt ggtatttaat cttcttccca tcatgtttga agtgatgctt 840
gtcagtggtg ttttgtatta caaatgcggg gccagtttg ctttggtaac ctttgaaca 900
cttggtacat acacagcatt cacagttgca gtcacacggg ggagaactag atttagaata 960
gaaatgaaca aagcagataa tgatgcaggt aatgctgcta tagactcact gctgaattat 1020

gaaactgtga agtatttttaa taatgaaaga tatgaagcac agagatatga tggatttttg	1080
aagacgtatg agactgcttc attgaaaagt acctctactc tggctatgct gaactttgggt	1140
caaagtgccta ttttcagtgt cggtttaaca gctataatgg tgctcgccag tcagggaatg	1200
gtggcaggta cccttactgt tggagatcta gtaatgggtga atggactgct ttttcagctt	1260
tcattacccc tgaactttct gggaaactgta tatagagaga ctagacaagc actcatagat	1320
atgaacacct tgtttactct actcaaggta gacacccaaa ttaaagacaa agtgatggca	1380
tctccccttc agatcacacc acagacagct accgtggcct ttgataatgt gcattttgaa	1440
tacattgagg gccagaaagt ccttagtgga atatccttg aagtcctgc aggaaagaaa	1500
gtggccattg taggaggtag tgggtcaggg aaaagcacia tagtgaggct attatttcgc	1560
ttctatgagc ctcaaaagg tagcatttat cttgctggtc aaaatataca agatgtgagc	1620
ctggaaagcc ttcggagggc agtgggagt gtacctcagg atgctgtcct cttccataat	1680
actatttatt acaacctctt atatggaaac atcagtgcct cacctgagga agtgtatgca	1740
gtggcaaaat tagctggact tcatgatgca attcttcgaa tgccacatgg atatgacacc	1800
caagtagggg aacgaggact caagctttca ggaggagaaa agcaaagagt agcaattgca	1860
agagccattt tgaaggaccc ccagtcata ctctatgatg aagctacttc atcgtttagat	1920
tcgattactg aagagactat tcttggtgcc atgaaggatg tgggtcaaaca cagaacttct	1980
attttcattg cacacagatt gtcaacagtg gttgatgcag atgaaatcat tgtcttggat	2040
cagggttaagg tagccgaacg tggtagccac catggtttgc ttgctaacct tcatagtatc	2100
tattcagaaa tgtggcatat acagagcagc cgtgtgcaga accatgataa ccccaaatgg	2160
gaagcaaaga aagaaaatat atccaaagag gaggaaagaa agaaactaca agaagaaatt	2220
gtcaatagtg tgaaaggctg tggaaactgt tcgtgctaag tcacataaga cattttcttt	2280
ttttgttggt ttggactaca tatttgcact gaagcagaat tgttttatta aaaaaatcat	2340
acatt	2345

<210> 4
 <211> 747
 <212> PRT
 <213> Homo sapien

 <400> 4

Met	His	Ser	Trp	Arg	Trp	Ala	Ala	Ala	Ala	Ala	Ala	Phe	Glu	Lys	Arg
1				5				10						15	

Arg His Ser Ala Ile Leu Ile Arg Pro Leu Val Ser Val Ser Gly Ser
 20 25 30

Gly Pro Gln Trp Arg Pro His Gln Leu Gly Ala Leu Gly Thr Ala Arg
 35 40 45

Ala Tyr Gln Ile Pro Glu Ser Leu Lys Ser Ile Thr Trp Gln Arg Leu
 50 55 60

Gly Lys Gly Asn Ser Gly Gln Phe Leu Asp Ala Ala Lys Ala Leu Gln
 65 70 75 80

Val Trp Pro Leu Ile Glu Lys Arg Thr Cys Trp His Gly His Ala Gly
 85 90 95

Gly Gly Leu His Thr Asp Pro Lys Glu Gly Leu Lys Asp Val Asp Thr
 100 105 110

Arg Lys Ile Ile Lys Ala Met Leu Ser Tyr Val Trp Pro Lys Asp Arg
 115 120 125

Pro Asp Leu Arg Ala Arg Val Ala Ile Ser Leu Gly Phe Leu Gly Gly
 130 135 140

Ala Lys Ala Met Asn Ile Val Val Pro Phe Met Phe Lys Tyr Ala Val
 145 150 155 160

Asp Ser Leu Asn Gln Met Ser Gly Asn Met Leu Asn Leu Ser Asp Ala
 165 170 175

Pro Asn Thr Val Ala Thr Met Ala Thr Ala Val Leu Ile Gly Tyr Gly
 180 185 190

Val Ser Arg Ala Gly Ala Ala Phe Phe Asn Glu Val Arg Asn Ala Val
 195 200 205

Phe Gly Lys Val Ala Gln Asn Ser Ile Arg Arg Ile Ala Lys Asn Val
 210 215 220

Phe Leu His Leu His Asn Leu Asp Leu Gly Phe His Leu Ser Arg Gln
 225 230 235 240

Thr Gly Ala Leu Ser Lys Ala Ile Asp Arg Gly Thr Lys Gly Ile Ser
245 250 255

Phe Val Leu Ser Ala Leu Val Phe Asn Leu Leu Pro Ile Met Phe Glu
260 265 270

Val Met Leu Val Ser Gly Val Leu Tyr Tyr Lys Cys Gly Ala Gln Phe
275 280 285

Ala Leu Val Thr Leu Gly Thr Leu Gly Thr Tyr Thr Ala Phe Thr Val
290 295 300

Ala Val Thr Arg Trp Arg Thr Arg Phe Arg Ile Glu Met Asn Lys Ala
305 310 315 320

Asp Asn Asp Ala Gly Asn Ala Ala Ile Asp Ser Leu Leu Asn Tyr Glu
325 330 335

Thr Val Lys Tyr Phe Asn Asn Glu Arg Tyr Glu Ala Gln Arg Tyr Asp
340 345 350

Gly Phe Leu Lys Thr Tyr Glu Thr Ala Ser Leu Lys Ser Thr Ser Thr
355 360 365

Leu Ala Met Leu Asn Phe Gly Gln Ser Ala Ile Phe Ser Val Gly Leu
370 375 380

Thr Ala Ile Met Val Leu Ala Ser Gln Gly Met Val Ala Gly Thr Leu
385 390 395 400

Thr Val Gly Asp Leu Val Met Val Asn Gly Leu Leu Phe Gln Leu Ser
405 410 415

Leu Pro Leu Asn Phe Leu Gly Thr Val Tyr Arg Glu Thr Arg Gln Ala
420 425 430

Leu Ile Asp Met Asn Thr Leu Phe Thr Leu Leu Lys Val Asp Thr Gln
435 440 445

Ile Lys Asp Lys Val Met Ala Ser Pro Leu Gln Ile Thr Pro Gln Thr
450 455 460

Ala Thr Val Ala Phe Asp Asn Val His Phe Glu Tyr Ile Glu Gly Gln
 465 470 475 480

Lys Val Leu Ser Gly Ile Ser Phe Glu Val Pro Ala Gly Lys Lys Val
 485 490 495

Ala Ile Val Gly Gly Ser Gly Ser Gly Lys Ser Thr Ile Val Arg Leu
 500 505 510

Leu Phe Arg Phe Tyr Glu Pro Gln Lys Gly Ser Ile Tyr Leu Ala Gly
 515 520 525

Gln Asn Ile Gln Asp Val Ser Leu Glu Ser Leu Arg Arg Ala Val Gly
 530 535 540

Val Val Pro Gln Asp Ala Val Leu Phe His Asn Thr Ile Tyr Tyr Asn
 545 550 555 560

Leu Leu Tyr Gly Asn Ile Ser Ala Ser Pro Glu Glu Val Tyr Ala Val
 565 570 575

Ala Lys Leu Ala Gly Leu His Asp Ala Ile Leu Arg Met Pro His Gly
 580 585 590

Tyr Asp Thr Gln Val Gly Glu Arg Gly Leu Lys Leu Ser Gly Gly Glu
 595 600 605

Lys Gln Arg Val Ala Ile Ala Arg Ala Ile Leu Lys Asp Pro Pro Val
 610 615 620

Ile Leu Tyr Asp Glu Ala Thr Ser Ser Leu Asp Ser Ile Thr Glu Glu
 625 630 635 640

Thr Ile Leu Gly Ala Met Lys Asp Val Val Lys His Arg Thr Ser Ile
 645 650 655

Phe Ile Ala His Arg Leu Ser Thr Val Val Asp Ala Asp Glu Ile Ile
 660 665 670

Val Leu Asp Gln Gly Lys Val Ala Glu Arg Gly Thr His His Gly Leu
 675 680 685

Leu Ala Asn Pro His Ser Ile Tyr Ser Glu Met Trp His Thr Gln Ser

690 695 700
 Ser Arg Val Gln Asn His Asp Asn Pro Lys Trp Glu Ala Lys Lys Glu
 705 710 715 720
 Asn Ile Ser Lys Glu Glu Glu Arg Lys Lys Leu Gln Glu Glu Ile Val
 725 730 735
 Asn Ser Val Lys Gly Cys Gly Asn Cys Ser Cys
 740 745

<210> 5
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Reverse Primer

<400> 5
 tgcttcagtg caaatatgta gtc

23

<210> 6
 <211> 690
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 6

Met Leu Leu Leu Pro Arg Cys Pro Val Ile Gly Arg Ile Val Arg Ser
 1 5 10 15
 Lys Phe Arg Ser Gly Leu Ile Arg Asn His Ser Pro Val Ile Phe Thr
 20 25 30
 Val Ser Lys Leu Ser Thr Gln Arg Pro Leu Leu Phe Asn Ser Ala Val
 35 40 45
 Asn Leu Trp Asn Gln Ala Gln Lys Asp Ile Thr His Lys Lys Ser Val
 50 55 60
 Glu Gln Phe Ser Ser Ala Pro Lys Val Lys Thr Gln Val Lys Lys Thr
 65 70 75 80
 Ser Lys Ala Pro Thr Leu Ser Glu Leu Lys Ile Leu Lys Asp Leu Phe
 85 90 95

Arg Tyr Ile Trp Pro Lys Gly Asn Asn Lys Val Arg Ile Arg Val Leu
 100 105 110

Ile Ala Leu Gly Leu Leu Ile Ser Ala Lys Ile Leu Asn Val Gln Val
 115 120 125

Pro Phe Phe Phe Lys Gln Thr Ile Asp Ser Met Asn Ile Ala Trp Asp
 130 135 140

Asp Pro Thr Val Ala Leu Pro Ala Ala Ile Gly Leu Thr Ile Leu Cys
 145 150 155 160

Tyr Gly Val Ala Arg Phe Gly Ser Val Leu Phe Gly Glu Leu Arg Asn
 165 170 175

Ala Val Phe Ala Lys Val Ala Gln Asn Ala Ile Arg Thr Val Ser Leu
 180 185 190

Gln Thr Phe Gln His Leu Met Lys Leu Asp Leu Gly Trp His Leu Ser
 195 200 205

Arg Gln Thr Gly Gly Leu Thr Arg Ala Met Asp Arg Gly Thr Lys Gly
 210 215 220

Ile Ser Gln Val Leu Thr Ala Met Val Phe His Ile Ile Pro Ile Ser
 225 230 235 240

Phe Glu Ile Ser Val Val Cys Gly Ile Leu Thr Tyr Gln Phe Gly Ala
 245 250 255

Ser Phe Ala Ala Ile Thr Phe Ser Thr Met Leu Leu Tyr Ser Ile Phe
 260 265 270

Thr Ile Lys Thr Thr Ala Trp Arg Thr His Phe Arg Arg Asp Ala Asn
 275 280 285

Lys Ala Asp Asn Lys Ala Ala Ser Val Ala Leu Asp Ser Leu Ile Asn
 290 295 300

Phe Glu Ala Val Lys Tyr Phe Asn Asn Glu Lys Tyr Leu Ala Asp Lys
 305 310 315 320

Tyr Asn Gly Ser Leu Met Asn Tyr Arg Asp Ser Gln Ile Lys Val Ser
325 330 335

Gln Ser Leu Ala Phe Leu Asn Ser Gly Gln Asn Leu Ile Phe Thr Thr
340 345 350

Ala Leu Thr Ala Met Met Tyr Met Gly Cys Thr Gly Val Ile Gly Gly
355 360 365

Asn Leu Thr Val Gly Asp Leu Val Leu Ile Asn Gln Leu Val Phe Gln
370 375 380

Leu Ser Val Pro Leu Asn Phe Leu Gly Ser Val Tyr Arg Asp Leu Lys
385 390 395 400

Gln Ser Leu Ile Asp Met Glu Thr Leu Phe Lys Leu Arg Lys Asn Glu
405 410 415

Val Lys Ile Lys Asn Ala Glu Arg Pro Leu Met Leu Pro Glu Asn Val
420 425 430

Pro Tyr Asp Ile Thr Phe Glu Asn Val Thr Phe Gly Tyr His Pro Asp
435 440 445

Arg Lys Ile Leu Lys Asn Ala Ser Phe Thr Ile Pro Ala Gly Trp Lys
450 455 460

Thr Ala Ile Val Gly Ser Ser Gly Ser Gly Lys Ser Thr Ile Leu Lys
465 470 475 480

Leu Val Phe Arg Phe Tyr Asp Pro Glu Ser Gly Arg Ile Leu Ile Asn
485 490 495

Gly Arg Asp Ile Lys Glu Tyr Asp Ile Asp Ala Leu Arg Lys Val Ile
500 505 510

Gly Val Val Pro Gln Asp Thr Pro Leu Phe Asn Asp Thr Ile Trp Glu
515 520 525

Asn Val Lys Phe Gly Arg Ile Asp Ala Thr Asp Glu Glu Val Ile Thr
530 535 540

Val Val Glu Lys Ala Gln Leu Ala Pro Leu Ile Lys Lys Leu Pro Gln

545		550		555		560									
Gly	Phe	Asp	Thr	Ile	Val	Gly	Glu	Arg	Gly	Leu	Met	Ile	Ser	Gly	Gly
				565					570					575	
Glu	Lys	Gln	Arg	Leu	Ala	Ile	Ala	Arg	Val	Leu	Leu	Lys	Asn	Ala	Arg
			580					585					590		
Ile	Met	Phe	Phe	Asp	Glu	Ala	Thr	Ser	Ala	Leu	Asp	Thr	His	Thr	Glu
		595						600				605			
Gln	Ala	Leu	Leu	Arg	Thr	Ile	Arg	Asp	Asn	Phe	Thr	Ser	Gly	Ser	Arg
	610					615					620				
Thr	Ser	Val	Tyr	Ile	Ala	His	Arg	Leu	Arg	Thr	Ile	Ala	Asp	Ala	Asp
625					630					635				640	
Lys	Ile	Ile	Val	Leu	Asp	Asn	Gly	Arg	Val	Arg	Glu	Glu	Gly	Lys	His
			645					650						655	
Leu	Glu	Leu	Leu	Ala	Met	Pro	Gly	Ser	Leu	Tyr	Arg	Glu	Leu	Trp	Thr
			660					665					670		
Ile	Gln	Glu	Asp	Leu	Asp	His	Leu	Glu	Asn	Glu	Leu	Lys	Asp	Gln	Gln
		675						680				685			
Glu	Leu														
	690														